

5040



PCT10

RAW SEQUENCE LISTING

DATE: 02/08/2002

PATENT APPLICATION: US/10/030,522

TIME: 11:35:47

Input Set : A:\522_1769.ST25.txt

Output Set: N:\CRF3\02082002\J030522.raw

ENTERED

3 <110> APPLICANT: Leuven Research & Development vzw
 4 Jacquemin, Marc G
 5 Saint-Remy, Jean-Marie R
 7 <120> TITLE OF INVENTION: Ligands for use in therapeutic compositions for the
 8 treatment of hemostatis disorders
 10 <130> FILE REFERENCE: K1564-PCT
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/030,522
 C--> 12 <141> CURRENT FILING DATE: 2001-12-31
 12 <150> PRIOR APPLICATION NUMBER: GB9916450.1
 13 <151> PRIOR FILING DATE: 1999-07-14
 15 <150> PRIOR APPLICATION NUMBER: US 60/143,891
 16 <151> PRIOR FILING DATE: 1999-07-14
 18 <160> NUMBER OF SEQ ID NOS: 8
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 143
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Homo sapiens
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 32 Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Phe Pro Gly Thr Leu Ser
 33 20 25 30
 36 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
 37 35 40 45
 40 Val Ala Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
 41 50 55 60
 44 Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro
 45 65 70 75 80
 48 His Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 49 85 90 95
 52 Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
 53 100 105 110
 56 Gly Thr Ser Ala Leu Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 57 115 120 125
 60 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
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 65 <211> LENGTH: 150
 66 <212> TYPE: PRT
 67 <213> ORGANISM: Homo sapiens
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71 1          5          10          15
74 Thr His Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
75          20          25          30
78 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu
79          35          40          45
82 Thr Glu Leu Pro Val His Trp Val Gly Gln Ala Pro Gly Lys Gly Leu
83          50          55          60
86 Glu Trp Val Gly Ser Phe Asp Pro Glu Ser Gly Glu Ser Ile Tyr Ala
87 65          70          75          80
90 Arg Glu Phe Gln Gly Ser Val Thr Met Thr Ala Asp Thr Ser Thr Asp
91          85          90          95
94 Ile Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val
95          100          105          110
98 Tyr Tyr Cys Ala Val Pro Asp Pro Asp Ala Phe Asp Ile Trp Gly Gln
99          115          120          125
102 Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
103          130          135          140
106 Phe Pro Leu Gly Ser Arg
107 145          150

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110 <210> SEQ ID NO: 3

111 <211> LENGTH: 142

112 <212> TYPE: PRT

113 <213> ORGANISM: Homo sapiens

W--> 114 <400> SEQUENCE: 3

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120 Asp Thr Thr Gly Glu Ile Ala Leu Thr Gln Ser Pro Gly Thr Leu Ser
121          20          25          30
124 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
125          35          40          45
128 Phe Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
129          50          55          60
132 Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro
133 65          70          75          80
136 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
137          85          90          95
140 Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Lys Tyr
141          100          105          110
144 Gly Thr Ser Ala Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
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153 <211> LENGTH: 429

154 <212> TYPE: DNA

155 <213> ORGANISM: Homo sapiens

157 <220> FEATURE:

158 <221> NAME/KEY: V_region

159 <222> LOCATION: (1)..(429)

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169 <222> LOCATION: (205)..(225)
170 <223> OTHER INFORMATION: complementary determining region number two
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173 <221> NAME/KEY: misc_feature
174 <222> LOCATION: (325)..(354)
175 <223> OTHER INFORMATION: complementary determining region number three
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180 gaaattgtgt tgacgcagtt cccaggcacc ctgtctttgt ctccagggga aagagccacc      120
182 ctctcctgca gggccagtc gagtggtgcc agcgctact tagcctggta ccagcaaaaa      180
184 cctggccagg ctcccaggct cctcatctat ggtgcatcca gtagggccac cgacatccca      240
186 cacaggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag      300
188 cctgaagatt ttgcagtgta ctactgtcag caatatggta cctcagcctt actcaacttc      360
190 ggcgaggagg ccaaggtgga gatcaaacga actgtggctg caccatctgt ctcatcttc      420
192 ccgccatct                                     429
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196 <211> LENGTH: 450
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202 <222> LOCATION: (1)..(450)
203 <223> OTHER INFORMATION:
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206 <221> NAME/KEY: misc_feature
207 <222> LOCATION: (130)..(159)
208 <223> OTHER INFORMATION: complementary determining region number one
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211 <221> NAME/KEY: misc_feature
212 <222> LOCATION: (202)..(258)
213 <223> OTHER INFORMATION: complementary determining region number two
215 <220> FEATURE:
216 <221> NAME/KEY: misc_feature
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223 gtccaactgg tacagtctgg ggctgagggt aagaagcctg gggcctcagt gaaggctctcc      120
225 tgcaagggtt ccggtatacac cctcactgaa ttaccgtgc actgggtcgg acaggctcct      180
227 ggaaaagggc ttgagtgggt gggaaagttt gatcctgaaa gtggagaatc aatctacgca      240
229 cgggagttcc agggcagcgt caccatgacc gcggacacat ctacagacat agcctacatg      300
231 gagctgagca gcctgagatc tgacgacacg gccgtgtatt actgtgcagt ccctgaccct      360

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235 ggcccatcgg tcttccccct gggatcccgt 450
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239 <211> LENGTH: 426
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243 <220> FEATURE:
244 <221> NAME/KEY: V_region
245 <222> LOCATION: (1)..(426)
246 <223> OTHER INFORMATION:
248 <220> FEATURE:
249 <221> NAME/KEY: misc_feature
250 <222> LOCATION: (7)..(162)
251 <223> OTHER INFORMATION: complementary determining region number one
253 <220> FEATURE:
254 <221> NAME/KEY: misc_feature
255 <222> LOCATION: (205)..(225)
256 <223> OTHER INFORMATION: complementary determining region number two
258 <220> FEATURE:
259 <221> NAME/KEY: misc_feature
260 <222> LOCATION: (325)..(351)
261 <223> OTHER INFORMATION: complementary determining region number three
263 <400> SEQUENCE: 6
264 atggaaaccc cagctcagct tctcttcctc ctgctactct ggtcccaga taccaccgga 60
266 gaaattgcgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 120
268 ctctcctgca gggccagtca gagtttttagc agcagctact tagcctggta tcagcagaaa 180
270 cctggccagg ctcccaggct cctcatctat ggtgcatcca ccagggccac tggcatccca 240
272 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 300
274 cctgaagatt ttgcagtgtg ttactgtcag aagtatggta cgtcagcgat caccttcggg 360
276 caagggacac gactggagat taaaggaact gtggctgcac catctgtctt catcttccc 420
278 ccatct 426
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282 <211> LENGTH: 468
283 <212> TYPE: DNA
284 <213> ORGANISM: Homo sapiens
286 <220> FEATURE:
287 <221> NAME/KEY: V_region
288 <222> LOCATION: (1)..(468)
289 <223> OTHER INFORMATION:
291 <220> FEATURE:
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293 <222> LOCATION: (124)..(192)
294 <223> OTHER INFORMATION: complementary determining region number one
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297 <221> NAME/KEY: misc_feature
298 <222> LOCATION: (232)..(285)
299 <223> OTHER INFORMATION: complementary determining region number two
301 <220> FEATURE:
302 <221> NAME/KEY: misc_feature

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Input Set : A:\522_1769.ST25.txt

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311 tgcaagacct ctggatacaa cttcaccggc tactctgctt ctggacatat cttcaccgcc      180
313 tactctgtgc actgggtgcg acaggcccct ggacaagggc ttgagtggat gggaaggatc      240
315 aaccctaaca gtggtgccac agactatgca cataaatttc agggcagggt caccatgtcc      300
317 agggacacgt ccatcagcac agcctacatg gaactgagca ggctgacatc tgacgacacg      360
319 gccatgtatt actgtgcgag agccgacaac tatttcgata ttgtgactgg ctatacttct      420
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324 <211> LENGTH: 156
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326 <213> ORGANISM: Homo sapiens
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333 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
334          20          25          30
337 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Asn Phe
338          35          40          45
341 Thr Gly Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His
342          50          55          60
345 Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile
346 65          70          75          80
349 Asn Pro Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg
350          85          90          95
353 Val Thr Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu
354          100         105         110
357 Ser Arg Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala
358          115         120         125
361 Asp Asn Tyr Phe Asp Ile Val Thr Gly Tyr Thr Ser His Tyr Phe Asp
362          130         135         140
365 Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
366 145         150         155

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VERIFICATION SUMMARY

DATE: 02/08/2002

PATENT APPLICATION: US/10/030,522

TIME: 11:35:48

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:68 M:283 W: Missing Blank Line separator, <400> field identifier
L:114 M:283 W: Missing Blank Line separator, <400> field identifier